



SEQUENCE LISTING

<110> Covacci, Antonello
Bugnoli, Massimo
Telford, John
Macchia, Giovanni
Rappuoli, Rino

<120> Helicobacter Pylori Cytotoxin Proteins Useful For
Vaccines And Diagnostics

<130> CHIR0158

<140> 09/360,934

<141> 1999-07-26

<160> 8

<170> PatentIn Ver. 2.1

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<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Artificial
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<212> DNA

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<223> Description of Artificial Sequence: Artificial
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<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificial Sequence

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Ala Ala Phe Phe Thr Thr Val Ile Ile Pro Ala Ile Val Gly Gly Ile
 35 40 45

Ala Thr Gly Thr Ala Val Gly Thr Val Ser Gly Leu Leu Ser Trp Gly
 50 55 60

Leu Lys Gln Ala Glu Glu Ala Asn Lys Thr Pro Asp Lys Pro Asp Lys
 65 70 75 80

Val Trp Arg Ile Gln Ala Gly Lys Gly Phe Asn Glu Phe Pro Asn Lys
 85 90 95

Glu Tyr Asp Leu Tyr Arg Ser Leu Leu Ser Ser Lys Ile Asp Gly Gly
 100 105 110

Trp Asp Trp Gly Asn Ala Ala Arg His Tyr Trp Val Lys Gly Gly Gln
 115 120 125

Gln Asn Lys Leu Glu Val Asp Met Lys Asp Ala Val Gly Thr Tyr Thr
 130 135 140

Leu Ser Gly Leu Arg Asn Phe Thr Gly Gly Asp Leu Asp Val Asn Met
 145 150 155 160

Gln Lys Ala Thr Leu Arg Leu Gly Gln Phe Asn Gly Asn Ser Phe Thr
 165 170 175

Ser Tyr Lys Asp Ser Ala Asp Arg Thr Thr Arg Val Asp Phe Asn Ala
 180 185 190

Lys Asn Ile Ser Ile Asp Asn Phe Val Glu Ile Asn Asn Arg Val Gly
 195 200 205

Ser Gly Ala Gly Arg Lys Ala Ser Ser Thr Val Leu Thr Leu Gln Ala
 210 215 220

Ser Glu Gly Ile Thr Ser Asp Lys Asn Ala Glu Ile Ser Leu Tyr Asp
 225 230 235 240

Gly Ala Thr Leu Asn Leu Ala Ser Ser Ser Val Lys Leu Met Gly Asn
 245 250 255

Val Trp Met Gly Arg Leu Gln Tyr Val Gly Ala Tyr Leu Ala Pro Ser
 260 265 270

Tyr Ser Thr Ile Asn Thr Ser Lys Val Thr Gly Glu Val Asn Phe Asn
 275 280 285

His Leu Thr Val Gly Asp Lys Asn Ala Ala Gln Ala Gly Ile Ile Ala
 290 295 300

Asn Lys Lys Thr Asn Ile Gly Thr Leu Asp Leu Trp Gln Ser Ala Gly
 305 310 315 320

Leu Asn Ile Ile Ala Pro Pro Glu Gly Gly Tyr Lys Asp Lys Pro Asn
 325 330 335

Asn Thr Pro Ser Gln Ser Gly Ala Lys Asn Asp Lys Asn Glu Ser Ala
 340 345 350

Lys Asn Asp Lys Gln Glu Ser Ser Gln Asn Asn Ser Asn Thr Gln Val
 355 360 365

Ile Asn Pro Pro Asn Ser Ala Gln Lys Thr Glu Val Gln Pro Thr Gln
 370 375 380

Val Ile Asp Gly Pro Phe Ala Gly Gly Lys Asp Thr Val Val Asn Ile
 385 390 395 400

Asn Arg Ile Asn Thr Asn Ala Asp Gly Thr Ile Arg Val Gly Gly Phe
 405 410 415

Lys Ala Ser Leu Thr Thr Asn Ala Ala His Leu His Ile Gly Lys Gly
 420 425 430

Gly Val Asn Leu Ser Asn Gln Ala Ser Gly Arg Ser Leu Ile Val Glu
 435 440 445

Asn Leu Thr Gly Asn Ile Thr Val Asp Gly Pro Leu Arg Val Asn Asn
 450 455 460

Gln Val Gly Gly Tyr Ala Leu Ala Gly Ser Ser Ala Asn Phe Glu Phe
 465 470 475 480

Lys Ala Gly Thr Asp Thr Lys Asn Gly Thr Ala Thr Phe Asn Asn Asp
 485 490 495

Ile Ser Leu Gly Arg Phe Val Asn Leu Lys Val Asp Ala His Thr Ala
 500 505 510

Asn Phe Lys Gly Ile Asp Thr Gly Asn Gly Gly Phe Asn Thr Leu Asp
 515 520 525

Phe Ser Gly Val Thr Asp Lys Val Asn Ile Asn Lys Leu Ile Thr Ala
 530 535 540

Ser Thr Asn Val Ala Val Lys Asn Phe Asn Ile Asn Glu Leu Ile Val
 545 550 555 560

Lys Thr Asn Gly Ile Ser Val Gly Glu Tyr Thr His Phe Ser Glu Asp
 565 570 575

Ile Gly Ser Gln Ser Arg Ile Asn Thr Val Arg Leu Glu Thr Gly Thr
 580 585 590

Arg Ser Leu Phe Ser Gly Gly Val Lys Phe Lys Gly Gly Glu Lys Leu
 595 600 605

Val Ile Asp Glu Phe Tyr Tyr Ser Pro Trp Asn Tyr Phe Asp Ala Arg
 610 615 620

Asn Ile Lys Asn Val Glu Ile Thr Asn Lys Leu Ala Phe Gly Pro Gln
 625 630 635 640

Gly	Ser	Pro	Trp	Gly	Thr	Ser	Lys	Leu	Met	Phe	Asn	Asn	Leu	Thr	Leu	645	650	655	
Gly	Gln	Asn	Ala	Val	Met	Asp	Tyr	Ser	Gln	Phe	Ser	Asn	Leu	Thr	Ile	660	665	670	
Gln	Gly	Asp	Phe	Ile	Asn	Asn	Gln	Gly	Thr	Ile	Asn	Tyr	Leu	Val	Arg	675	680	685	
Gly	Gly	Lys	Val	Ala	Thr	Leu	Ser	Val	Gly	Asn	Ala	Ala	Ala	Met	Met	690	695	700	
Phe	Asn	Asn	Asp	Ile	Asp	Ser	Ala	Thr	Gly	Phe	Tyr	Lys	Pro	Leu	Ile	705	710	715	720
Lys	Ile	Asn	Ser	Ala	Gln	Asp	Leu	Ile	Lys	Asn	Thr	Glu	His	Val	Leu	725	730	735	
Leu	Lys	Ala	Lys	Ile	Ile	Gly	Tyr	Gly	Asn	Val	Ser	Thr	Gly	Thr	Asn	740	745	750	
Gly	Ile	Ser	Asn	Val	Asn	Leu	Glu	Glu	Gln	Phe	Lys	Glu	Arg	Leu	Ala	755	760	765	
Leu	Tyr	Asn	Asn	Asn	Asn	Arg	Met	Asp	Thr	Cys	Val	Val	Arg	Asn	Thr	770	775	780	
Asp	Asp	Ile	Lys	Ala	Cys	Gly	Met	Ala	Ile	Gly	Asp	Gln	Ser	Met	Val	785	790	795	800
Asn	Asn	Pro	Asp	Asn	Tyr	Lys	Tyr	Leu	Ile	Gly	Lys	Ala	Trp	Lys	Asn	805	810	815	
Ile	Gly	Ile	Ser	Lys	Thr	Ala	Asn	Gly	Ser	Lys	Ile	Ser	Val	Tyr	Tyr	820	825	830	
Leu	Gly	Asn	Ser	Thr	Pro	Thr	Glu	Asn	Gly	Gly	Asn	Thr	Thr	Asn	Leu	835	840	845	
Pro	Thr	Asn	Thr	Thr	Ser	Asn	Ala	Arg	Ser	Ala	Asn	Asn	Ala	Leu	Ala	850	855	860	
Gln	Asn	Ala	Pro	Phe	Ala	Gln	Pro	Ser	Ala	Thr	Pro	Asn	Leu	Val	Ala	865	870	875	880
Ile	Asn	Gln	His	Asp	Phe	Gly	Thr	Ile	Glu	Ser	Val	Phe	Glu	Leu	Ala	885	890	895	

Asn Arg Ser Lys Asp Ile Asp Thr Leu Tyr Ala Asn Ser Gly Ala Gln
 900 905 910

Gly Arg Asp Leu Leu Gln Thr Leu Leu Ile Asp Ser His Asp Ala Gly
 915 920 925

Tyr Ala Arg Lys Met Ile Asp Ala Thr Ser Ala Asn Glu Ile Thr Lys
 930 935 940

Gln Leu Asn Thr Ala Thr Thr Thr Leu Asn Asn Ile Ala Ser Leu Glu
 945 950 955 960

His Lys Thr Ser Gly Leu Gln Thr Leu Ser Leu Ser Asn Ala Met Ile
 965 970 975

Leu Asn Ser Arg Leu Val Asn Leu Ser Arg Arg His Thr Asn His Ile
 980 985 990

Asp Ser Phe Ala Lys Arg Leu Gln Ala Leu Lys Asp Gln Lys Phe Ala
 995 1000 1005

Ser Leu Glu Ser Ala Ala Glu Val Leu Tyr Gln Phe Ala Pro Lys Tyr
 1010 1015 1020

Glu Lys Pro Thr Asn Val Trp Ala Asn Ala Ile Gly Gly Thr Ser Leu
 1025 1030 1035 1040

Asn Asn Gly Ser Asn Ala Ser Leu Tyr Gly Thr Ser Ala Gly Val Asp
 1045 1050 1055

Ala Tyr Leu Asn Gly Gln Val Glu Ala Ile Val Gly Gly Phe Gly Ser
 1060 1065 1070

Tyr Gly Tyr Ser Ser Phe Asn Asn Arg Ala Asn Ser Leu Asn Ser Gly
 1075 1080 1085

Ala Asn Asn Thr Asn Phe Gly Val Tyr Ser Arg Ile Phe Ala Asn Gln
 1090 1095 1100

His Glu Phe Asp Phe Glu Ala Gln Gly Ala Leu Gly Ser Asp Gln Ser
 1105 1110 1115 1120

Ser Leu Asn Phe Lys Ser Ala Leu Leu Gln Asp Leu Asn Gln Ser Tyr
 1125 1130 1135

His Tyr Leu Ala Tyr Ser Ala Ala Thr Arg Ala Ser Tyr Gly Tyr Asp
 1140 1145 1150

Phe Ala Phe Phe Arg Asn Ala Leu Val Leu Lys Pro Ser Val Gly Val
1155 1160 1165

Ser Tyr Asn His Leu Gly Ser Thr Asn Phe Lys Ser Asn Ser Thr Asn
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Gln Val Ala Leu Lys Asn Gly Ser Ser Ser Gln His Leu Phe Asn Ala
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Ser Ala Asn Val Glu Ala Arg Tyr Tyr Tyr Gly Asp Thr Ser Tyr Phe
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Tyr Met Asn Ala Gly Val Leu Gln Glu Phe Ala His Val Gly Ser Asn
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Asn Ala Ala Ser Leu Asn Thr Phe Lys Val Asn Ala Ala Arg Asn Pro
1235 1240 1245

Leu Asn Thr His Ala Arg Val Met Met Gly Gly Glu Leu Lys Leu Ala
1250 1255 1260

Lys Glu Val Phe Leu Asn Leu Gly Val Val Tyr Leu His Asn Leu Ile
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<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificial
Sequence

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aactctgtaa	aatccctatt	atagggacac	agagtggaaa	ccaaactctc	cctacgggca	4260
acatcagcct	aggaagccca	atcgtcttta	gcggttgggc	acttcacctt	aaaatatccc	4320
gacagacact	aacgaaaggc	tttgttcttt	aaagtctgca	tggatatattc	ctaccccaaa	4380
aagacttaac	cctttgctta	aaattaagtt	tgattgtgct	agtgggttcg	tgctatagt	4440
cgaaaattaa	ttaaggggta	taaagagagc	ataaactaga	aaaaacaagt	agctataaca	4500
aagatcaagt	tcaaaaaatc	atagagcttt	tagagcaaat	tgatcgcgct	cttaaccaaa	4560
gaaaaatcag	aaaaaccata	ggaattatca	caccttataa	tgcccaaaaa	agacgcttgc	4620
gatcagaagt	ggaaaaatac	ggcttcaaga	attttgatga	gctcaaaata	gacactgtgg	4680
atgcctttca	aggtgaagag	gcagatatta	ttatttatcc	caccgtgaaa	acttgtggta	4740
atctttcttt	cttgctagat	tctaaacgct	tgaatgtggc	tatttctagg	gcaaaaagaaa	4800
atctcatttt	tgtgggtaaa	aagtctttct	ttgagaattt	atgaagcgat	gagaagaata	4860
tcttttagcg	tattttgcaa	gtctgtagat	aggtaatctt	ttccaaagat	aatcattaga	4920
cattcttcgc	ttcaaaacgc	tttcataaat	ctctctaaag	cgctttataa	tcaacacaat	4980
acccttatag	tgtgagctat	agcccttttt	tgggaattga	gttattttga	ctttaaattt	5040
ttattagcgt	tacaatttga	gccattcttt	agcttggttt	tctagccaga	tcacatcgcc	5100
gctcgcatga	aattccactt	tagggaatgc	gtgtgcattt	tttttaagg	cgatattttg	5160
ctgcaaatat	cctacaatat	catcgcccga	atggatgagt	agggggggtg	ttgaaagggc	5220
aaaatgctcc	ataaaatagc	cctcaatttt	ttgagcgatt	aagggaataa	gcgtgcaacc	5280
taaaataatc	acttcgggaa	aatctttaag	ggagtgaat	aataacgcat	gcaagtttct	5340
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tgcgaaacat	tcaaatagcc	ttgttggttc	agggcattgt	cataagcggt	ggattggatc	5460
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tctaaagcta	gagcgctcgc	tgtgttgcat	gccacaatca	ataattcaat	ctgggtcggt	5640
ttgaaaaaat	ccaaagcctc	taagccaaat	tgcttgatcg	tagtggggtc	tttagtgcca	5700
taaggcactc	tagccgtatc	gccataatag	atgatttcat	caaataattg	cgctttttaa	5760
aggcttttta	aaacgctaaa	ccctcccaca	ccgctatcaa	aaacgcctat	tttcatgaca	5820
cttttttaat	ttaatgggat	taattaggga	ttttattttt	cattcattaa	gtttaaaaat	5880
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<211> 1147

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificial
Sequence

<400> 5

Met Thr Asn Glu Thr Ile Asp Gln Gln Pro Gln Thr Glu Ala Ala Phe
1 5 10 15

Asn Pro Gln Gln Phe Ile Asn Asn Leu Gln Val Ala Phe Leu Lys Val
20 25 30

Asp Asn Ala Val Ala Ser Tyr Asp Pro Asp Gln Lys Pro Ile Val Asp
35 40 45

Lys Asn Asp Arg Asp Asn Arg Gln Ala Phe Glu Gly Ile Ser Gln Leu
50 55 60

Arg Glu Glu Tyr Ser Asn Lys Ala Ile Lys Asn Pro Thr Lys Lys Asn
65 70 75 80

Gln Tyr Phe Ser Asp Phe Ile Asn Lys Ser Asn Asp Leu Ile Asn Lys
85 90 95

Asp Asn Leu Ile Asp Val Glu Ser Ser Thr Lys Ser Phe Gln Lys Phe
100 105 110

Gly Asp Gln Arg Tyr Arg Ile Phe Thr Ser Trp Val Ser His Gln Asn
115 120 125

Asp Pro Ser Lys Ile Asn Thr Arg Ser Ile Arg Asn Phe Met Glu Asn
130 135 140

Ile Ile Gln Pro Pro Ile Leu Asp Asp Lys Glu Lys Ala Glu Phe Leu
145 150 155 160

Lys Ser Ala Lys Gln Ser Phe Ala Gly Ile Ile Ile Gly Asn Gln Ile
165 170 175

Arg Thr Asp Gln Lys Phe Met Gly Val Phe Asp Glu Ser Leu Lys Glu
180 185 190

Arg Gln Glu Ala Glu Lys Asn Gly Glu Pro Thr Gly Gly Asp Trp Leu
195 200 205

Asp Ile Phe Leu Ser Phe Ile Phe Asp Lys Lys Gln Ser Ser Asp Val
 210 215 220

Lys Glu Ala Ile Asn Gln Glu Pro Val Pro His Val Gln Pro Asp Ile
 225 230 235 240

Ala Thr Thr Thr Thr Asp Ile Gln Gly Leu Pro Pro Glu Ala Arg Asp
 245 250 255

Leu Leu Asp Glu Arg Gly Asn Phe Ser Lys Phe Thr Leu Gly Asp Met
 260 265 270

Glu Met Leu Asp Val Glu Gly Val Ala Asp Ile Asp Pro Asn Tyr Lys
 275 280 285

Phe Asn Gln Leu Leu Ile His Asn Asn Ala Leu Ser Ser Val Leu Met
 290 295 300

Gly Ser His Asn Gly Ile Glu Pro Glu Lys Val Ser Leu Leu Tyr Gly
 305 310 315 320

Gly Asn Gly Gly Pro Gly Ala Arg His Asp Trp Asn Ala Thr Val Gly
 325 330 335

Tyr Lys Asp Gln Gln Gly Asn Asn Val Ala Thr Ile Ile Asn Val His
 340 345 350

Met Lys Asn Gly Ser Gly Leu Val Ile Ala Gly Gly Glu Lys Gly Ile
 355 360 365

Asn Asn Pro Ser Phe Tyr Leu Tyr Lys Glu Asp Gln Leu Thr Gly Ser
 370 375 380

Gln Arg Ala Leu Ser Gln Glu Glu Ile Gln Asn Lys Ile Asp Phe Met
 385 390 395 400

Glu Phe Leu Ala Gln Asn Asn Ala Lys Leu Asp Asn Leu Ser Glu Lys
 405 410 415

Glu Lys Glu Lys Phe Arg Thr Glu Ile Lys Asp Phe Gln Lys Asp Ser
 420 425 430

Lys Ala Tyr Leu Asp Ala Leu Gly Asn Asp Arg Ile Ala Phe Val Ser
 435 440 445

Lys Lys Asp Thr Lys His Ser Ala Leu Ile Thr Glu Phe Gly Asn Gly
 450 455 460

Asp	Leu	Ser	Tyr	Thr	Leu	Lys	Asp	Tyr	Gly	Lys	Lys	Ala	Asp	Lys	Ala	
465					470					475					480	
Leu	Asp	Arg	Glu	Lys	Asn	Val	Thr	Leu	Gln	Gly	Ser	Leu	Lys	His	Asp	
				485					490					495		
Gly	Val	Met	Phe	Val	Asp	Tyr	Ser	Asn	Phe	Lys	Tyr	Thr	Asn	Ala	Ser	
			500					505					510			
Lys	Asn	Pro	Asn	Lys	Gly	Val	Gly	Val	Thr	Asn	Gly	Val	Ser	His	Leu	
		515					520					525				
Glu	Val	Gly	Phe	Asn	Lys	Val	Ala	Ile	Phe	Asn	Leu	Pro	Asp	Leu	Asn	
	530					535					540					
Asn	Leu	Ala	Ile	Thr	Ser	Phe	Val	Arg	Arg	Asn	Leu	Glu	Asp	Lys	Leu	
545					550					555					560	
Thr	Thr	Lys	Gly	Leu	Ser	Pro	Gln	Glu	Ala	Asn	Lys	Leu	Ile	Lys	Asp	
				565					570					575		
Phe	Leu	Ser	Ser	Asn	Lys	Glu	Leu	Val	Gly	Lys	Thr	Leu	Asn	Phe	Asn	
			580					585					590			
Lys	Ala	Val	Ala	Asp	Ala	Lys	Asn	Thr	Gly	Asn	Tyr	Asp	Glu	Val	Lys	
		595					600					605				
Lys	Ala	Gln	Lys	Asp	Leu	Glu	Lys	Ser	Leu	Arg	Lys	Arg	Glu	His	Leu	
	610					615				620						
Glu	Lys	Glu	Val	Glu	Lys	Lys	Leu	Glu	Ser	Lys	Ser	Gly	Asn	Lys	Asn	
625					630					635				640		
Lys	Met	Glu	Ala	Lys	Ala	Gln	Ala	Asn	Ser	Gln	Lys	Asp	Glu	Ile	Phe	
				645					650					655		
Ala	Leu	Ile	Asn	Lys	Glu	Ala	Asn	Arg	Asp	Ala	Arg	Ala	Ile	Ala	Tyr	
			660					665					670			
Ala	Gln	Asn	Leu	Lys	Gly	Ile	Lys	Arg	Glu	Leu	Ser	Asp	Lys	Leu	Glu	
		675					680					685				
Asn	Val	Asn	Lys	Asn	Leu	Lys	Asp	Phe	Asp	Lys	Ser	Phe	Asp	Glu	Phe	
	690					695					700					
Lys	Asn	Gly	Lys	Asn	Lys	Asp	Phe	Ser	Lys	Ala	Glu	Glu	Thr	Leu	Lys	
705					710					715				720		

Ala	Leu	Lys	Gly	Ser	Val	Lys	Asp	Leu	Gly	Ile	Asn	Pro	Glu	Trp	Ile	725	730	735	
Ser	Lys	Val	Glu	Asn	Leu	Asn	Ala	Ala	Leu	Asn	Glu	Phe	Lys	Asn	Gly	740	745	750	
Lys	Asn	Lys	Asp	Phe	Ser	Lys	Val	Thr	Gln	Ala	Lys	Ser	Asp	Leu	Glu	755	760	765	
Asn	Ser	Val	Lys	Asp	Val	Ile	Ile	Asn	Gln	Lys	Val	Thr	Asp	Lys	Val	770	775	780	
Asp	Asn	Leu	Asn	Gln	Ala	Val	Ser	Val	Ala	Lys	Ala	Thr	Gly	Asp	Phe	785	790	795	800
Ser	Arg	Val	Glu	Gln	Ala	Leu	Ala	Asp	Leu	Lys	Asn	Phe	Ser	Lys	Glu	805	810	815	
Gln	Leu	Ala	Gln	Gln	Ala	Gln	Lys	Asn	Glu	Ser	Leu	Asn	Ala	Arg	Lys	820	825	830	
Lys	Ser	Glu	Ile	Tyr	Gln	Ser	Val	Lys	Asn	Gly	Val	Asn	Gly	Thr	Leu	835	840	845	
Val	Gly	Asn	Gly	Leu	Ser	Gln	Ala	Glu	Ala	Thr	Thr	Leu	Ser	Lys	Asn	850	855	860	
Phe	Ser	Asp	Ile	Lys	Lys	Glu	Leu	Asn	Ala	Lys	Leu	Gly	Asn	Phe	Asn	865	870	875	880
Asn	Asn	Asn	Asn	Asn	Gly	Leu	Lys	Asn	Glu	Pro	Ile	Tyr	Ala	Lys	Val	885	890	895	
Asn	Lys	Lys	Lys	Ala	Gly	Gln	Ala	Ala	Ser	Leu	Glu	Glu	Pro	Ile	Tyr	900	905	910	
Ala	Gln	Val	Ala	Lys	Lys	Val	Asn	Ala	Lys	Ile	Asp	Arg	Leu	Asn	Gln	915	920	925	
Ile	Ala	Ser	Gly	Leu	Gly	Val	Val	Gly	Gln	Ala	Ala	Gly	Phe	Pro	Leu	930	935	940	
Lys	Arg	His	Asp	Lys	Val	Asp	Asp	Leu	Ser	Lys	Val	Gly	Leu	Ser	Arg	945	950	955	960
Asn	Gln	Glu	Leu	Ala	Gln	Lys	Ile	Asp	Asn	Leu	Asn	Gln	Ala	Val	Ser	965	970	975	

Glu Ala Lys Ala Gly Phe Phe Gly Asn Leu Glu Gln Thr Ile Asp Lys
980 985 990

Leu Lys Asp Ser Thr Lys His Asn Pro Met Asn Leu Trp Val Glu Ser
995 1000 1005

Ala Lys Lys Val Pro Ala Ser Leu Ser Ala Lys Leu Asp Asn Tyr Ala
1010 1015 1020

Thr Asn Ser His Ile Arg Ile Asn Ser Asn Ile Lys Asn Gly Ala Ile
1025 1030 1035 1040

Asn Glu Lys Ala Thr Gly Met Leu Thr Gln Lys Asn Pro Glu Trp Leu
1045 1050 1055

Lys Leu Val Asn Asp Lys Ile Val Ala His Asn Val Gly Ser Val Pro
1060 1065 1070

Leu Ser Glu Tyr Asp Lys Ile Gly Phe Asn Gln Lys Asn Met Lys Asp
1075 1080 1085

Tyr Ser Asp Ser Phe Lys Phe Ser Thr Lys Leu Asn Asn Ala Val Lys
1090 1095 1100

Asp Thr Asn Ser Gly Phe Thr Gln Phe Leu Thr Asn Ala Phe Ser Thr
1105 1110 1115 1120

Ala Ser Tyr Tyr Cys Leu Ala Arg Glu Asn Ala Glu His Gly Ile Lys
1125 1130 1135

Asn Val Asn Thr Lys Gly Gly Phe Gln Lys Ser
1140 1145

<210> 6

<211> 546

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificial
Sequence

<400> 6

Met Ala Lys Glu Ile Lys Phe Ser Asp Ser Ala Arg Asn Leu Leu Phe
1 5 10 15

Glu Gly Val Arg Gln Leu His Asp Ala Val Lys Val Thr Met Gly Pro

20	25	30
Arg Gly Arg Asn Val Leu Ile Gln Lys Ser Tyr Gly Ala Pro Ser Ile		
35	40	45
Thr Lys Asp Gly Val Ser Val Ala Lys Glu Ile Glu Leu Ser Cys Pro		
50	55	60
Val Ala Asn Met Gly Ala Gln Leu Val Lys Glu Val Ala Ser Lys Thr		
65	70	75
Ala Asp Ala Ala Gly Asp Gly Thr Thr Thr Ala Thr Val Leu Ala Tyr		
85	90	95
Ser Ile Phe Lys Glu Gly Leu Arg Asn Ile Thr Ala Gly Ala Asn Pro		
100	105	110
Ile Glu Val Lys Arg Gly Met Asp Lys Ala Ala Glu Ala Ile Ile Asn		
115	120	125
Glu Leu Lys Lys Ala Ser Lys Lys Val Gly Gly Lys Glu Glu Ile Thr		
130	135	140
Gln Val Ala Thr Ile Ser Ala Asn Ser Asp His Asn Ile Gly Lys Leu		
145	150	155
Ile Ala Asp Ala Met Glu Lys Val Gly Lys Asp Gly Val Ile Thr Val		
165	170	175
Glu Glu Ala Lys Gly Ile Glu Asp Glu Leu Asp Val Val Glu Gly Met		
180	185	190
Gln Phe Asp Arg Gly Tyr Leu Ser Pro Tyr Phe Val Thr Asn Ala Glu		
195	200	205
Lys Met Thr Ala Gln Leu Asp Asn Ala Tyr Ile Leu Leu Thr Asp Lys		
210	215	220
Lys Ile Ser Ser Met Lys Asp Ile Leu Pro Leu Leu Glu Lys Thr Met		
225	230	235
Lys Glu Gly Lys Pro Leu Leu Ile Ile Ala Glu Asp Ile Glu Gly Glu		
245	250	255
Ala Leu Thr Thr Leu Val Val Asn Lys Leu Arg Gly Val Leu Asn Ile		
260	265	270
Ala Ala Val Lys Ala Pro Gly Phe Gly Asp Arg Arg Lys Glu Met Leu		

275	280	285
Lys Asp Ile Ala Ile Leu Thr Gly Gly Gln Val Ile Ser Glu Glu Leu		
290	295	300
Gly Leu Ser Leu Glu Asn Ala Glu Val Glu Phe Leu Gly Lys Ala Gly		
305	310	315 320
Arg Ile Val Ile Asp Lys Asp Asn Thr Thr Ile Val Asp Gly Lys Gly		
325	330	335
His Ser Asp Asp Val Lys Asp Arg Val Ala Gln Ile Lys Thr Gln Ile		
340	345	350
Ala Ser Thr Thr Ser Asp Tyr Asp Lys Glu Lys Leu Gln Glu Arg Leu		
355	360	365
Ala Lys Leu Ser Gly Gly Val Ala Val Ile Lys Val Gly Ala Ala Ser		
370	375	380
Glu Val Glu Met Lys Glu Lys Lys Asp Arg Val Asp Asp Ala Leu Ser		
385	390	395 400
Ala Thr Lys Ala Ala Val Glu Glu Gly Ile Val Ile Gly Gly Gly Ala		
405	410	415
Ala Leu Ile Arg Ala Ala Gln Lys Val His Leu Asn Leu His Asp Asp		
420	425	430
Glu Lys Val Gly Tyr Glu Ile Ile Met Arg Ala Ile Lys Ala Pro Leu		
435	440	445
Ala Gln Ile Ala Ile Asn Ala Gly Tyr Asp Gly Gly Val Val Val Asn		
450	455	460
Glu Val Glu Lys His Glu Gly His Phe Gly Phe Asn Ala Ser Asn Gly		
465	470	475 480
Lys Tyr Val Asp Met Phe Lys Glu Gly Ile Ile Asp Pro Leu Lys Val		
485	490	495
Glu Arg Ile Ala Leu Gln Asn Ala Val Ser Val Ser Ser Leu Leu Leu		
500	505	510
Thr Thr Glu Ala Thr Val His Glu Ile Lys Glu Glu Lys Ala Thr Pro		
515	520	525
Ala Met Pro Asp Met Gly Gly Met Gly Gly Met Gly Gly Met Gly Gly		

Met Met
545

<210> 7
<211> 1838
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Artificial
Sequence

<400> 7
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gcaaaagaaa tcaaattttc agatagtgcg agaaaccttt tatttgaagg cgtgaggcaa 120
ctccatgacg ctgtcaaagt aaccatgggg ccaagaggca ggaatgtatt gatccaaaaa 180
agctatggcg ctccaagcat caccaaagac ggcgtagcg tggctaaaga gattgaatta 240
agttgcccag tagctaacat gggcgctcaa ctcgttaaag aagtagcgag caaaaccgct 300
gatgctgccg gcgatggcac gaccacagcg accgtgctag cttatagcat ttttaaagaa 360
ggtttgagga atatcacggc tggggctaac cctattgaag tgaaacgagg catggataaa 420
gctgctgaag cgatcattaa tgagcttaaa aaagcgagca aaaaagtagg cggtaaagaa 480
gaaatcacc aagtggcgac catttctgca aactccgac acaatatcg gaaactcatc 540
gctgacgcta tggaaaaagt gggtaaaagc ggcgtagca ccgttgagga agctaagggc 600
attgaagatg aattggatgt cgtagaaggc atgcaatttg atagaggcta cctctccct 660
tattttgtaa cgaacgctga gaaaatgacc gctcaatttg ataagtctta catcctttta 720
acggataaaa aaatctctag catgaaagac attctccgc tactagaaaa aaccatgaaa 780
gagggcaaac cgcttttaat catcgctgaa gacattgagg gcgaagcttt aacgactcta 840
gtggtgaata aattaagagg cgtgttgaat atcgacgagg ttaaagctcc aggctttggg 900
gacagaagaa aagaaatgct caaagacatc gctattttta ccggcggtca agtcattagc 960
gaagaattgg gcttgagtct agaaaacgct gaagtggagt ttttaggcaa agctggaagg 1020
attgtgattg acaaagacaa caccacgac gtagatggca aaggccatag cgatgatgtt 1080
aaagacagag tcgcgcagat caaaaccaa attgcaagta cgacaagcga ttatgacaaa 1140
gaaaaattgc aagaaagatt ggctaaactc tctggcgggtg tggctgtgat taaagtgggc 1200
gctgcgagtg aagtggaaat gaaagagaaa aaagaccggg tggatgacgc gttgagcgcg 1260
actaaagcgg cggttgaaga aggcattgtg attggtggcg gtgcggctct cattcgcgcg 1320
gctcaaaaag tgcatttgaa ttgcacgat gatgaaaaag tgggctatga aatcatcatg 1380
cgcgccatta aagccccatt agctcaaact gctatcaacg ctggttatga tggcggtgtg 1440
gtcgtgaatg aagtagaaaa acacgaaggg cattttgggt ttaacgctag caatggcaag 1500
tatgtggata tgttttaaaga aggcattatt gacccttaa aagtagaaag gatcgctcta 1560
caaatgctgg tttcggtttc aagcctgctt ttaaccacag aagccaccgt gcatgaaatc 1620
aaagaagaaa aagcgactcc ggcaatgcct gatatgggtg gcatgggcgg tatgggaggc 1680
atgggcggca tgatgtaagc ccgcttgctt ttagtataaa tctgctttta aaatcccttc 1740
tctaaatccc cccctttcta aaatctcttt tttggggggg tgctttgata aaaccgctcg 1800
cttgtaaaaa catgcaacaa aaatctctg ttaagctt 1838

<210> 8
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Artificial
Sequence

<400> 8
gactcgagtc gacatcga

18